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line from the bottom, reference is made to "inventions I-IX below". However, only Groups I-V are seen. Confirmation is requested that, in fact, only Groups I-V were intended. Further, on page 2 of the Action, line 5 of the first full paragraph, and, on page 3 of the Action, line 6, reference is made to Groups I-VII. Here too, confirmation is requested that only Groups I-V were intended. Finally, it is assumed that Group I was intended to encompass claims 1-46 rather than claims 1-13 and 28-46. Were this not to be the case, claims 14-27 would not be present in any Group - confirmation is requested.

With the foregoing assumption regarding Group I in mind, Applicants elect the subject matter of Group I for prosecution in this application. This election is made with traverse. If claims 14-27 are not included in Group I, the Examiner is requested to issue a new Action properly reciting claims 14-27 and setting a new date for response.

In response to the Examiner's requirement for election of a specific sequence, Applicants elect the sequence of SEQ ID NO:104. (It is noted that no explanation is provided that would serve to justify such a requirement.) This election too is made with traverse. The Examiner is requested to reconsider and withdraw the requirement for

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restriction to a single sequence. To require such restriction is unfairly burdensome to Applicants from the standpoint of the enormous number of divisional applications that would be required. Further, such a requirement, as it is understood, may preclude Applicants from receiving an Action on the merits of a claim that encompasses the entirety of the subject invention. Should the Examiner refuse Applicants' request to reconsider and withdraw, or at least restructure, the requirement, Applicants request that the undersigned be so notified before the first Action on the merits is issued so that a Petition can be filed requesting withdrawal/restructuring of the requirement.

In traversing the requirement for restriction, Applicants urge the Examiner to take into account the following comments.

Rule 13.1 PCT states:

'The international application shall relate to one invention only or to a group of inventions so linked as to form a single general inventive concept'.

All the present claims, in particular all the sequences disclosed, fall within a single inventive concept (as evidenced by the presence of the same or a

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corresponding special technical feature) as defined by Rule 13 PCT.

Rule 13.2 PCT 1st sentence states:

'Where a group of inventions is claimed in one and the same international application. the requirement of unity of invention referred to in Rule 13.1PCT shall be fulfilled only when there is a technical relationship among those inventions involving one or more of the same or corresponding technical features'.

Rule 13.2 PCT 2nd sentence states:

'The expression " special technical features" shall mean those technical features that define a contribution which each of the claimed inventions considered as a whole, makes over the prior art'.

Thus, where there exists the same or a corresponding feature which defines the contribution made by the invention over the prior art as defined by Rule 13.2 PCT 2nd sentence, there exists a single inventive concept which confers unity of invention under Rule 13.1 PCT.

The *Rht* phenotype is a particular dwarf phenotype in wheat which is known in the art. The corresponding phenotype has also been characterized in other plants such as maize, where it is known as D8/D9 (see page 3, line 27- page 4, line 17, of the present application).

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The nucleotide sequences set out in the present application are responsible for the *Rht* dwarf phenotype or its equivalent in other plants. Applicants have discovered that a particular sequence element which is responsible for the gibberellin interaction is an important characteristic of the wild type sequences. The identification of this element enables homologues from other species to be cloned and also allows plant responses to gibberellin to be manipulated.

The provision of the nucleotide sequences responsible for the *Rht* phenotype or its equivalent in other plants are corresponding special technical features which are reflected in all the present claims. Sequences which reflect these corresponding special technical features may be wild type and lead to a normal phenotype or may be mutants and lead to the *Rht* phenotype. These features reflect the contribution made over the art since none of these gene sequences has previously been described (i.e. they are not present in the art).

All the present claims therefore relate to a single inventive concept and fulfill the requirements for unity under Rule 13 PCT.

Many dwarf phenotypes have been identified in plants. Two particular dwarf phenotypes in maize are described in

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Haberd et al (1989). A phenotype is however not an isolated gene. While the existence of a particular phenotype may be attributed to a genetic mutation, it provides no information about the molecular basis of that mutation. The practice in the art of naming the gene after the known phenotype is not an indication that the gene was known at the time the phenotype was identified.

Chaing et al (WO96/05317) describes the molecular basis of the GA4 phenotype and discloses a protein and a nucleotide sequence. This Arabidopsis dwarf phenotype is one of a group of known gibberellin sensitive phenotypes (GA1, GA2, GA3, GA4, and GA5: see page 1 of Peng et al (1993) The Plant Cell 5 351-360). The addition of exogenous gibberellin to mutants of this type overcomes the phenotype. Page 21, line 2, and page 10, lines 13-17, of Chaing et al confirm that GA4 mutants are gibberellin sensitive. Thus, they are distinct from the *Rht*-type dwarf mutants described in the present application, which are gibberellin insensitive.

The unity of the subject-matter of the present application is not therefore affected by the disclosures of the cited prior art documents.

Groups II - V relate to methods of identifying *Rht* polynucleotide, isolated *Rht* polypeptide, antibody which

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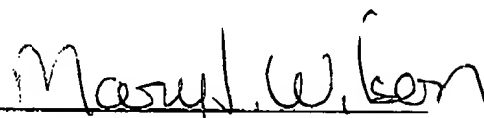
'binds Rht polypeptide and methods of identifying Rht polypeptide. All these groupings possess a special technical feature which corresponds to that described above (i.e. an Rht polypeptide or encoding nucleotide) and are therefore part of the same inventive concept as Group I.

An early and favorable Action on the merits is requested.

Respectfully submitted,

NIXON & VANDERHYE, P.C.

By



Mary J. Wilson
Reg. No. 32,955

MJW:tat

1100 North Glebe Road
8th Floor
Arlington, Virginia 22201-4714
Telephone: (703) 816-4000
Facsimile: (703) 816-4100